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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,461

DATE: 12/26/2001

TIME: 16:22:42

Input Set : N:\Crf3\RULE60\09879461.txt

Output Set: N:\CRF3\12262001\I879461.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Holmes, Stephen D.  
 6 Gross, Mitchell S.  
 7 Sylvester, Daniel R.  
 9 (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 10 Treatment of IL4 Mediated Disorders  
 12 (iii) NUMBER OF SEQUENCES: 58  
 14 (iv) CORRESPONDENCE ADDRESS:  
 15 (A) ADDRESSEE: SmithKline Beecham Corporation  
 16 (B) STREET: Corporate Intellectual Property, UW2220 - 709  
 17 Swedeland Rd.  
 18 (C) CITY: King of Prussia  
 19 (D) STATE: PA  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 19406-2799  
 23 (v) COMPUTER READABLE FORM:  
 24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 29 (vi) CURRENT APPLICATION DATA:  
 C--> 30 (A) APPLICATION NUMBER: US/09/879,461  
 C--> 31 (B) FILING DATE: 12-Jun-2001  
 32 (C) CLASSIFICATION:  
 34 (vii) PRIOR APPLICATION DATA:  
 35 (A) APPLICATION NUMBER: 08/612,929  
 36 (B) FILING DATE:  
 38 (A) APPLICATION NUMBER: US 08/136,783  
 39 (B) FILING DATE: 14-OCT-1993  
 41 (viii) ATTORNEY/AGENT INFORMATION:  
 42 (A) NAME: Sutton, Jeffrey A.  
 43 (B) REGISTRATION NUMBER: 34,028  
 44 (C) REFERENCE/DOCKET NUMBER: P50186-2  
 46 (ix) TELECOMMUNICATION INFORMATION:  
 47 (A) TELEPHONE: (215) 270-5024  
 48 (B) TELEFAX: (215) 270-5090  
 52 (2) INFORMATION FOR SEQ ID NO: 1:  
 54 (i) SEQUENCE CHARACTERISTICS:  
 55 (A) LENGTH: 396 base pairs  
 56 (B) TYPE: nucleic acid  
 57 (C) STRANDEDNESS: double  
 58 (D) TOPOLOGY: unknown  
 60 (ii) MOLECULE TYPE: cDNA  
 62 (ix) FEATURE:  
 63 (A) NAME/KEY: CDS  
 64 (B) LOCATION: 1..396

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71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA      48
74 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
75   1           5           10           15
77 GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT      96
78 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
79           20           25           30
81 GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT      144
82 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
83           35           40           45
85 GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA      192
86 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
87   50           55           60
89 GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT      240
90 Gly Gln Pro Pro Lys Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
91  65           70           75           80
93 GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC      288
94 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
95           85           90           95
97 CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT      336
98 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
99   100           105           110
101 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG      384
102 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
103   115           120           125
105 GAA ATC AAA CGG      396
106 Glu Ile Lys Arg
107   130
110 (2) INFORMATION FOR SEQ ID NO: 2:
112      (i) SEQUENCE CHARACTERISTICS:
113          (A) LENGTH: 132 amino acids
114          (B) TYPE: amino acid
115          (D) TOPOLOGY: linear
117      (ii) MOLECULE TYPE: protein
119      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
122   1           5           10           15
124 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
125           20           25           30
127 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
128           35           40           45
130 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
131           50           55           60
134 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
135  65           70           75           80
137 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
138           85           90           95
140 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
141   100           105           110

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143 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
144      115                      120                      125
146 Glu Ile Lys Arg
147      130
150 (2) INFORMATION FOR SEQ ID NO: 3:
152     (i) SEQUENCE CHARACTERISTICS:
153         (A) LENGTH: 483 base pairs
154         (B) TYPE: nucleic acid
155         (C) STRANDEDNESS: double
156         (D) TOPOLOGY: unknown
158     (ii) MOLECULE TYPE: cDNA
160     (ix) FEATURE:
161         (A) NAME/KEY: CDS
162         (B) LOCATION: 64..483
164     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
166 GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA      60
168 GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA      108
169 Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala
170      1      5      10      15
172 TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG      156
173 Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
174      20      25      30
176 CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA      204
177 Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
178      35      40      45
180 CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA      252
181 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
182      50      55      60
184 AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC      300
185 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
186      65      70      75
188 TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC      348
189 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
190      80      85      90      95
192 AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT      396
193 Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
194      100      105      110
197 GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC      444
198 Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
199      115      120      125
201 GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA      483
202 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
203      130      135      140
206 (2) INFORMATION FOR SEQ ID NO: 4:
208     (i) SEQUENCE CHARACTERISTICS:
209         (A) LENGTH: 140 amino acids
210         (B) TYPE: amino acid
211         (D) TOPOLOGY: linear
213     (ii) MOLECULE TYPE: protein

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215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

217 Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr
218   1           5           10           15
220 Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
221           20           25           30
223 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
224           35           40           45
226 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
227           50           55           60
229 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
230   65           70           75           80
232 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
233           85           90           95
235 Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
236           100          105          110
238 Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
239           115          120          125
241 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
242   130          135          140

```

245 (2) INFORMATION FOR SEQ ID NO: 5:

247 (i) SEQUENCE CHARACTERISTICS:

248 (A) LENGTH: 60 base pairs

249 (B) TYPE: nucleic acid

250 (C) STRANDEDNESS: double

251 (D) TOPOLOGY: unknown

253 (ii) MOLECULE TYPE: cDNA

255 (ix) FEATURE:

256 (A) NAME/KEY: CDS

257 (B) LOCATION: 1..60

260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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262 ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT      48
263 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
264   1           5           10           15
266 GGT GCC TAC GGG      60
267 Gly Ala Tyr Gly
268           20

```

271 (2) INFORMATION FOR SEQ ID NO: 6:

273 (i) SEQUENCE CHARACTERISTICS:

274 (A) LENGTH: 20 amino acids

275 (B) TYPE: amino acid

276 (D) TOPOLOGY: linear

278 (ii) MOLECULE TYPE: protein

280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

282 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
283   1           5           10           15
285 Gly Ala Tyr Gly
286           20

```

289 (2) INFORMATION FOR SEQ ID NO: 7:

291 (i) SEQUENCE CHARACTERISTICS:

## RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\09879461.txt

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292      (A) LENGTH: 57 base pairs
293      (B) TYPE: nucleic acid
294      (C) STRANDEDNESS: double
295      (D) TOPOLOGY: unknown
297      (ii) MOLECULE TYPE: cDNA
299      (ix) FEATURE:
300          (A) NAME/KEY: CDS
301          (B) LOCATION: 1..57
303      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
305 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT      48
306 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
307   1              5              10              15
309 GTC CAC TCC      57
310 Val His Ser
314 (2) INFORMATION FOR SEQ ID NO: 8:
316      (i) SEQUENCE CHARACTERISTICS:
317          (A) LENGTH: 19 amino acids
318          (B) TYPE: amino acid
319          (D) TOPOLOGY: linear
321      (ii) MOLECULE TYPE: protein
323      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
325 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
326   1              5              10              15
328 Val His Ser
331 (2) INFORMATION FOR SEQ ID NO: 9:
333      (i) SEQUENCE CHARACTERISTICS:
334          (A) LENGTH: 423 base pairs
335          (B) TYPE: nucleic acid
336          (C) STRANDEDNESS: double
337          (D) TOPOLOGY: unknown
339      (ii) MOLECULE TYPE: cDNA
341      (ix) FEATURE:
342          (A) NAME/KEY: CDS
343          (B) LOCATION: 1..423
345      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
347 ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT      48
348 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
349   1              5              10              15
351 GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG      96
352 Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
353   20              25              30
355 CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA      144
356 Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
357   35              40              45
359 CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA      192
360 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
361   50              55              60
363 AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC      240
364 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg

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VERIFICATION SUMMARY

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TIME: 16:22:43

Input Set : N:\Crf3\RULE60\09879461.txt

Output Set: N:\CRF3\12262001\I879461.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]